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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 04:22:25 ; Search time 2763 Seconds
                                            (without alignments)
                                            15046.897 Million cell
updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc..........aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being
printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB ID   .   Description

1	828	96.5	1624	9	HUMERPR	M34986 Human eryth
2	828	96.5	1818	6	AX658275	AX658275 Sequence
3	828	96.5	1818	9	HUMERYTH	M60459 Human eryth
4	826.4	96.3	1527	6	AR062465	AR062465 Sequence
5	824.8	96.1	1317	6	AR202361	AR202361 Sequence
6	824.8	96.1	1317	6	AX008198	AX008198 Sequence
7	820	95.6	1317	6	AR202362	AR202362 Sequence
8	820	95.6	1317	6	AX008201	AX008201 Sequence
9	818.4	95.4	1848	6	CQ724319	CQ724319 Sequence
10	750.4	87.5	4990	6	AR119365	AR119365 Sequence
11	750	87.4	750	6	AR031378	AR031378 Sequence
12	750	87.4	750	6	BD134377	BD134377 Peptide 1
13	750	87.4	750	6	AR428937	AR428937 Sequence
14	750	87.4	750	6	BD009746	BD009746 Compositi
15	748.2	87.2	6256	6	BD168201	BD168201 Method of
16	741	86.4	5565	6	BD168199	BD168199 Method of
17	702	81.8	1666	6	BD090961	BD090961 Assay emp
18	610	71.1	1843	4	AF274305	AF274305 Sus scrof
19	577.6	67.3	2154	9	BC019092	BC019092 Homo sapi
20	577.6	67.3	5761	9	AK074082	AK074082 Homo sapi
21	576.4	67.2	5683	6	AX554424	AX554424 Sequence
22	576.4	67.2	6122	6	AX554413	AX554413 Sequence
23	576.4	67.2	6122	6	AX554422	AX554422 Sequence
24	576.4	67.2	6122	6	AX642149	AX642149 Sequence
25	576.4	67.2	6125	6	AX554420	AX554420 Sequence
26	576.2	67.2	1741	10	MUSERPR	J04843 Mouse eryth
27	576	67.1	4883	6	AX600116	AX600116 Sequence
28	574.6	67.0	1769	10	BC046282	BC046282 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 04:18:19 ; Search time 406 Seconds
                                        (without alignments)
                                        12510.192 Million cell
updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc..........aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being
printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description

1	828	96.5	1024	10	ABZ83469	Abz83469
Toxicolog						
2	828	96.5	1527	2	AAQ82990	Aaq82990
Human ery						
3	828	96.5	1733	10	ADE28670	Ade28670
Human NOV						
4	828	96.5	1733	10	ADE28672	Ade28672
Human NOV						
5	828	96.5	1733	12	ADM93417	Adm93417
Human NOV						
6	828	96.5	1733	12	ADM93415	Adm93415
Human NOV						
7	828	96.5	1848	13	ADQ83546	Adq83546
Human tum						
8	828	96.5	1849	12	ADO05723	Ado05723
Human ery						
9	828	96.5	1849	12	ADP10351	Adp10351
Reference						
10	828	96.5	1849	13	ACN40465	Acn40465
Tumour-as						
11	828	96.5	1883	2	AAQ05748	Aaq05748 EPO
recep						
12	826.4	96.3	1527	6	ABL51519	Abl51519
Human ery						
13	826.4	96.3	1818	2	AAQ81892	Aaq81892
Human ery						
14	824.8	96.1	1317	3	AAZ49634	Aaz49634
Truncated						
15	823.2	95.9	1585	10	ADE28676	Ade28676
Human NOV						
16	823.2	95.9	1585	12	ADM93421	Adm93421
Human NOV						
17	823.2	95.9	1818	2	AAQ53995	Aaq53995
Human EPO						
18	820	95.6	1317	3	AAZ49636	Aaz49636
Mutant R1						
19	820	95.6	1435	10	ADE28674	Ade28674
Human NOV						
20	820	95.6	1435	12	ADM93419	Adm93419
Human NOV						
21	750.4	87.5	4990	2	AAT48800	Aat48800
Plasmid m						
22	750	87.4	750	2	AAV04434	Aav04434
Erythropo						
23	750	87.4	750	2	AAZ30854	Aaz30854
Human ery						
24	748.2	87.2	6256	6	AAL43173	Aal43173
pCAGGS-hS						
25	741	86.4	5565	6	AAL43171	Aal43171
Human exp						
26	700.4	81.6	1666	2	AAX58148	Aax58148
CadC-fusi						
27	577.8	67.3	1740	2	AAQ05747	Aaq05747 EPO
recep						
28	576.4	67.2	5683	6	AAL41116	Aal41116
Plasmid p						

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 05:43:57 ; Search time 2386 Seconds
                                              (without alignments)
                                              13687.822 Million cell
updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc..........aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being
printed,
         and is derived by analysis of the total score distribution.

                            SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description

   ------
       1   828   96.5   1759 3   CR592865   CR592865
full-leng
       2   828   96.5   1797 3   CR620075   CR620075
full-leng

3	828	96.5	1811	3	CR618473	CR618473 full-leng
4	804	93.7	984	5	BX448344	BX448344 BX448344
5	795.4	92.7	1079	1	AL553257	AL553257 AL553257
6	788	91.8	1005	5	BX335579	BX335579 BX335579
7	756	88.1	1527	9	AY414846	AY414846 Homo sapi
8	737.2	85.9	997	1	AL523468	AL523468 AL523468
9	714	83.2	1870	3	CR610088	CR610088 full-leng
10	693.8	80.9	881	1	AL521907	AL521907 AL521907
11	645.8	75.3	1051	1	AL523895	AL523895 AL523895
12	630	73.4	902	1	AL523633	AL523633 AL523633
13	610.4	71.1	816	5	BX406158	BX406158 BX406158
14	577.6	67.3	1681	3	CR613702	CR613702 full-leng
15	543.6	63.4	1054	5	BX382171	BX382171 BX382171
16	501.4	58.4	1452	9	AY414848	AY414848 Mus muscu
17	487.8	56.9	853	5	BQ919762	BQ919762 AGENCOURT
18	446.8	52.1	1009	6	BY710355	BY710355 BY710355
19	446.8	52.1	1524	3	AK010968	AK010968 Mus muscu
20	418.8	48.8	482	5	BQ359730	BQ359730 RC4-HN004
21	397.8	46.4	1115	9	AY414847	AY414847 Pan trogl
22	345.8	40.3	658	6	BY752258	BY752258 BY752258
23	338.2	39.4	676	2	BE289169	BE289169 601092771
24	330.8	38.6	592	4	BI344043	BI344043 372394 MA
25	300.4	35.0	514	4	BI344106	BI344106 372470 MA
26	288.4	33.6	660	6	BY729758	BY729758 BY729758
27	285.8	33.3	350	1	AA218796	AA218796 zq97c05.r
c 28	283	33.0	1082	5	BX382170	BX382170 BX382170
29	256.2	29.9	383	2	BF661091	BF661091 maa79h04.
30	252	29.4	840	5	BX360123	BX360123 BX360123

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:30:07 ; Search time 507 Seconds
                                        (without alignments)
                                        11315.038 Million cell
updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc..........aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                   1:   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                   2:   /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                   3:   /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                   4:   /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                   5:   /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                   6:   /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                   7:   /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                   8:   /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                   9:   /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                   10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                   11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                   12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                   13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                   14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                   15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                   16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                   17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                   18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                   19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                   20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
                   21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
                   22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                   23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                   24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                   25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                   26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	858	100.0	858	19	US-10-625-137-4	Sequence 4, Appli
2	828	96.5	954	19	US-10-625-137-6	Sequence 6, Appli
3	828	96.5	987	19	US-10-625-137-8	Sequence 8, Appli
4	828	96.5	1733	18	US-10-287-971-47	Sequence 47, Appl
5	828	96.5	1733	18	US-10-287-971-49	Sequence 49, Appl
6	828	96.5	1818	10	US-09-960-706-693	Sequence 693, App
7	828	96.5	1818	21	US-10-482-029-191	Sequence 191, App
8	828	96.5	1849	21	US-10-684-206-23	Sequence 23, Appl
9	828	96.5	1865	19	US-10-625-137-3	Sequence 3, Appli
10	826.4	96.3	1527	9	US-09-016-159-4	Sequence 4, Appli
11	823.2	95.9	1585	18	US-10-287-971-53	Sequence 53, Appl
12	820	95.6	1435	18	US-10-287-971-51	Sequence 51, Appl
13	748.2	87.2	6256	18	US-10-432-305-3	Sequence 3, Appli
14	741	86.4	804	19	US-10-625-137-10	Sequence 10, Appl
15	741	86.4	5565	18	US-10-432-305-1	Sequence 1, Appli
16	739.8	86.2	747	19	US-10-625-137-12	Sequence 12, Appl
17	576.4	67.2	6122	14	US-10-006-591-1	Sequence 1, Appli
18	576	67.1	1056	19	US-10-134-188-30	Sequence 30, Appl
19	576	67.1	1059	19	US-10-134-188-29	Sequence 29, Appl
20	576	67.1	1121	19	US-10-134-188-26	Sequence 26, Appl
21	576	67.1	1131	19	US-10-134-188-25	Sequence 25, Appl
22	576	67.1	4883	14	US-10-006-593-111	Sequence 111, App

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.OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:15:47 ; Search time 141 Seconds
                                            (without alignments)
                                            9956.918 Million cell
updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc..........aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being
printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                     %
Result   Query
  No.   Score   Match Length DB   ID   Description

------
      1   828   96.5   1848   4   US-09-949-016-3882   Sequence
3882, Ap
      2   826.4   96.3   1527   2   US-08-850-293-4   Sequence 4,
Appli
      3   824.8   96.1   1317   3   US-09-339-838-4   Sequence 4,
Appli
      4   820   95.6   1317   3   US-09-339-838-6   Sequence 6,
Appli

5	750.4	87.5	4990	3	US-08-776-511-1	Sequence 1, Appli
6	750	87.4	750	2	US-08-627-151A-9	Sequence 9, Appli
7	750	87.4	750	4	US-09-646-691B-7	Sequence 7, Appli
8	702	81.8	1666	3	US-09-149-922-4	Sequence 4, Appli
9	576	67.1	1056	4	US-10-134-188-30	Sequence 30, Appl
10	576	67.1	1059	4	US-10-134-188-29	Sequence 29, Appl
11	576	67.1	1121	4	US-10-134-188-26	Sequence 26, Appl
12	576	67.1	1131	4	US-10-134-188-25	Sequence 25, Appl
13	523.4	61.0	774	2	US-08-762-308-9	Sequence 9, Appli
14	249	29.0	10546	4	US-09-949-016-15624	Sequence 15624, A
c 15	52.6	6.1	15447	4	US-09-902-540-1100	Sequence 1100, Ap
16	49.2	5.7	44377	2	US-08-804-227C-7	Sequence 7, Appli
17	49.2	5.7	44377	2	US-08-804-198-1	Sequence 1, Appli
18	49	5.7	1794	4	US-09-252-991A-5989	Sequence 5989, Ap
19	46.8	5.5	999	4	US-09-902-540-8482	Sequence 8482, Ap
c 20	46.8	5.5	7513	4	US-09-902-540-892	Sequence 892, App
c 21	46.4	5.4	289	3	US-09-007-005-17	Sequence 17, Appl
c 22	46.4	5.4	289	3	US-09-244-796-17	Sequence 17, Appl
23	46.4	5.4	2580	4	US-09-902-540-7003	Sequence 7003, Ap
c 24	46.4	5.4	4075	4	US-09-902-540-614	Sequence 614, App
c 25	46.2	5.4	243	4	US-09-252-991A-5899	Sequence 5899, Ap
26	45.8	5.3	1356	4	US-09-902-540-8249	Sequence 8249, Ap
27	45.8	5.3	6698	4	US-09-902-540-852	Sequence 852, App
c 28	45.6	5.3	1053	4	US-09-252-991A-13541	Sequence 13541, A
29	45.6	5.3	1557	4	US-09-252-991A-13907	Sequence 13907, A
30	45.6	5.3	1722	4	US-09-252-991A-13800	Sequence 13800, A
31	45.2	5.3	1926	3	US-09-249-585A-4	Sequence 4, Appli
32	45.2	5.3	1931	2	US-09-130-114-2	Sequence 2, Appli